ccccgccgtg agtgagctct caccccagtc agccaaatga gcctcttcgg gcttctcctg 60

gtgacatctg ccctggccgg ccagagacga gggactcagg cggaatccaa cctgagtagt 120

aaattccagt tttccagcaa caaggaacag aacggagtac aagatcctca gcatgagaga 180

attattactg tgtctactaa tggaagtatt cacagcccaa ggtttcctca tacttatcca 240

agaaatacgg tcttggtatg gagattagta gcagtagagg aaaatgtatg gatacaactt 300

acgtttgatg aaagatttgg gcttgaagac ccagaagatg acatatgcaa gtatgatttt 360

gtagaagttg aggaacccag tgatggaact atattagggc gctggtgtgg ttctggtact 420

gtaccaggaa aacagatttc taaaggaaat caaattagga taagatttgt atctgatgaa 480

tattttcctt ctgaaccagg gttctgcatc cactacaaca ttgtcatgcc acaattcaca 540

gaagctgtga gtccttcagt gctacccccc tcagctttgc cactggacct gcttaataat 600

gctataactg cctttagtac cttggaagac cttattcgat atcttgaacc agagagatgg 660

cagttggact tagaagatct atataggcca acttggcaac ttcttggcaa ggcttttgtt 720

tttggaagaa aatccagagt ggtggatctg aaccttctaa cagaggaggt aagattatac 780

agctgcacac ctcgtaactt ctcagtgtcc ataagggaag aactaaagag aaccgatacc 840

attttctggc caggttgtct cctggttaaa cgctgtggtg ggaactgtgc ctgttgtctc 900

cacaattgca atgaatgtca atgtgtccca agcaaagtta ctaaaaaata ccacgaggtc 960

cttcagttga gaccaaagac cggtgtcagg ggattgcaca aatcactcac cgacgtggcc 1020

ctggagcacc atgaggagtg tgactgtgtg tgcagaggga gcacaggagg atagccgcat 1080

caccaccagc agctcttgcc cafafctgtg cagtgcagtg gctgattcta ttagagaacg 1140

tatgcgttat ctccatcctt aatctcagtt gtttgcttca aggacctttc atcttcagga 1200

FIG. 1A

tttacagtgt attctgaaag aggagacatc aaacagaatt aggacttgtg caacagctct 1260

tttgagagga ggcctaaagg acaggagaaa aggtcttcaa tcgtggaaag aaaattaaat 1320

gttgtattaa atagatcacc agctagtttc agagtcacca tgtacgtatt ccactagctg 1380

ggttctgtat ttcagttctt tcgatacggc ttagggtaat gtcagtacag gaaaaaaact 1440

gtgcaagtga gcacctgatt ccgttgcctt gcttaactct aaagctccat gtcctgggcc 1500

taaaatcgta taaaatctgg attttttttt ttttttttgc tcatattcac atatgtaaac 1560

cagaacattc tatgtactac aaacctggtt tttaaaaagg aactatgttg ctatgaatta 1620

aacttgtgtc rtgctgatag gacagactgg attttttcata tttcttatta aaatttctgc 1680

catttagaag aagagaacta cattcatggt ttggaagaga taaacctgaa aagaagagtg 1740

gccttatcct cactttatcg ataagtgact ttatttgttt cattgtgtac atttttatat 1800

tctccttttg acattataac tgttggcttt tctaatcttg ttaaatatat ctatttttac 1860

caaaggtatt taatattctt ttttatgaca acttagatca actatttttа gcttggtaaa 1920

ttttttctaaa cacaattgtt atagccagag gaacaaagat ggatataaaa atattgttgc 1980

cctggacaaa aatacatgta tntccatccc ggaatggtgc tagagttgga ttaaacctgc 2040

attttaaaaa acctgaattg ggaanggaan ttggtaaggt tggccaaanc ttttttgaaa 2100

ataattaa 2108

FIG. 1B

Met Ser Keu Phe Gly Leu Leu Leu Cal Thr Ser Ala Leu Ala Gly Gln
1 5 10 15
Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
20 25 30
Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
35 40 45
Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
50 55 60
His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65 70 75 80
Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
85 90 95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Gly Asp Phe Val Glu Val Glu
100 105 110
Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
115 120 125
Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
130 135 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145 150 155 160
Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
165 170 175
Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
180 185 190
Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
195 200 205
Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
210 215 220
Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225 230 235 240
Leu thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
245 250 255
Val Ser Ile Arg Glu Glu Leu Lye Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
275 280 285

FIG. 2A

```
His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lsy Lys
    290                 295                 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Cal Arg Gly Leu
305                 310                 315                 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
                325                 330                 335
Cys Val Cys Arg Gly Ser Thr Gly Gly
            340                 345
```

FIG. 2B

cgggtaaatt ccagttttcc agcaacaagg aacagaacgg agtacaagat cctcagcatg 60
agagaattat tactgtgtct actaatggaa gtattcacag cccaaggttt cctcatactt 120
atccaagaaa tacggtcttg gtatggagat tagtagcagt agaggaaaat gtatggatac 180
aacttacgtt tgatgaaaga tttgggcttg aagacccaga agatgacata tgcaagtatg 240
attttgtaga agttgaggaa cccagtgatg gaactatatt agggcgctgg tgtggttctg 300
gtactgtacc aggaaaacag atttctaaag gaaatcaaat taggataaga tttgtatctg 360
atgaatattt tccttctgaa ccagggttct gcatccacta caacattgtc atgccacaat 420
tcacagaagc tgtgagtcct tcagtgctac ccccttcagc tttgccactg gacctgctta 480
ataatgctat aactgccttt agtaccttgg aagaccttat tcgatatctt gaaccagaga 540
gatggcagtt ggacttagaa gatctatata ggccaacttg gcaacttctt ggcaaggctt 600
ttgtttttgg aagaaaatcc agagtggtgg atctgaacct tctaacagag gaggtaagat 660
tatacagctg cacacctcgt aacttctcag tgtccataag ggaagaacta aagagaaccg 720
ataccatttt ctggccaggt tgtctcctgg ttaaacgctg tggtgggaac tgtgcctgtt 780
gtctccacaa ttgcaatgaa tgtcaatgtg tcccaagcaa agttactaaa aaataccacg 840
aggtccttca gttgagacca aasaccggtg tcaggggatt gcacaaatca ctcaccgacg 900
tggccctgga gcaccatgag gagtgtgact gtgtgtgtag agggagcaca ggaggatagc 960
cgcatcacca ccagcagctc ttgcccagag ctgtgcagtg cagtggctga ttctattaga 1020
gaacgtatgc gttatctcca tccttaatct cagttgtttg cttcaaggac ctttcatctt 1080
caggatttac agtgcattct gaaagaggag acatcaaaca gaattaggag ttgtgcaaca 1140
gctcttttga gaggaggcct aaaggacagg agaaaaggtc ttcaatcgtg gaaagaaaat 1200
taaatgttgt attaaataga tcaccagcta gtttcagagt taccatgtat gtattccact 1260
agctgggttc tgtatttcag ttctttcgat acggcttagg gtaatgtcag tacaggaaaa 1320
aaactgtgca agtgagcacc tgattccgtt gccttgctta actctaaagc tccatgtcct 1380
gggcctaaaa tcgtataaaa tctggatttt ttttttttt tttgctcata ttcacatatg 1440
taaaccagaa cattctatgt actacaaacc tggtttttaa aaaggaacta tgttgctatg 1500
aattaaactt gtgtcatgct gataggacag actgga 1536

FIG.3

```
Gly Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp
 1               5                  10                  15
Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His
            20                  25                  30
Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn The Val Leu Val Trp
        35                  40                  45
Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp
    50                  55                  60
Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp
65                  70                  75                  80
Phe Val Glu Val Glu Glu Pro Ser Asp Gly The Ile Leu Gly Arg Trp
                85                  90                  95
Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln
            100                 105                 110
Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly
        115                 120                 125
Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val
    130                 135                 140
Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn
145                 150                 155                 160
Asn Ale Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu
                165                 170                 175
Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr
            180                 185                 190
Trp Gln Leu Leu Glu Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val
        195                 200                 205
Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr
    210                 215                 220
Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp
225                 230                 235                 240
the Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn
                245                 250                 255
Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser
            260                 265                 270
Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr
        275                 280                 285
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His
    290                 295                 300
His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly
305                 310                 315
```

FIG.4

cacctggaga cacagaagag ggctctagga aaaattttgg atggggatta tgtggaaact 60
accctgcgat tctctgctgc cagagccggc caggcgcttc caccgcagcg cagcctttcc 120
ccgggctggg ctgagccttg gagtcgtcgc ttccccagtg cccgccgcga gtgagccctc 180
gccccagtca gccaaatgct cctcctcggc cctcctcggc ctcctcctgc gctggccggc 240
caaagaacgg ggactcgggc tgagtccaac ctgagcagca agttgcagct ctccagcgac 300
aaggaacaga acggagtgca agatccccgg catgagagag ttgtcactat atctggtaat 360
gggagcatcc acagcccgaa gtttcctcat acgtacccaa gaaatatggt gctggtgtgg 420
agattagttg cagtagatga tatagtgcgg atccagctga catttgatga gagatttggg 480
ctggaagatc cagaagacga tatatgcaag tatgattttg tagaagttga ggagcccagt 540
gatggaagtg ttttaggacg ctggtgtggt tctgggactg tgccaggaaa gcagacttct 600
aaaggaaatc atatcaggat aagatttgta tctgatgagt attttccatc tgaacccgga 660
ttctgcatcc actacagtat tatcatgcca caagtcacag aaaccacgag tccttcggtg 720
ttgccccctt catctttgtc attggacctg ctcaacaatg ctgtgactgc cttcagtacc 780
ttggaagagc tgattcggta cctagagcca gatcgatggc aggtggactt ggacagcctc 840
tacaagccaa catggcagct tttgggcaag gctttcctgt atgggaaaaa aagcaaagtg 900
gtgaatctga atctcctcaa ggaagaggta aaactctaca gctgcacacc ccggaacttc 960
tcagtgtcca tacgggaaga gctaaagagg acagatacca tattctggcc aggttgtttt 1020
ctggtcaagt gctgtggagg aaattgtgcc tgttgtctcc ataattgcaa tgaatgtcag 1080
tgtgtcccac gtaaagttac aaaaaagtac catgaggtcc ttcagttgag accaaaaact 1140
ggagtcaagg gattgcataa gtcactcact gatgtggctc tggaacacca cgaggaatgt 1200
gactgtgtgt gtagaggaaa cgcaggaggg taactgcagc cttcgtagca gcacacgtga 1260
gcactggcat tctgtgtacc cccacaagca accttcatcc ccaccagcgt tggccgcagg 1320
gctctcagct gctgatgctg gctatggtaa agatcttact cgtctccaac caaattctca 1380
gttgtttgct tcaatagcct tcccctgcag gacttcaagt gtcttctaaa agaccagagg 1440
caccaanagg agtcaatcac aaagcactgc accg 1474

FIG.5

```
Met Leu Leu Leu Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
 1               5                  10                  15
Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
            20                  25                  30
Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
        35                  40                  45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
    50                  55                  60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65                  70                  75                  80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                85                  90                  95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                 105                 110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                 120                 125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
    130                 135                 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                 160
Ser Ile Ile Met Pro Gln ValThr Glu Thr Thr Ser Pro Ser Val Leu
                165                 170                 175
Pro Pro Ser Ser Leu Ser Lei Asp Leu Leu Asn Asn Ala Val Thr Ala
            180                 185                 190
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
        195                 200                 205
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
    210                 215                 220
Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225                 230                 235                 240
Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
                245                 250                 255
Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
            260                 265                 270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
        275                 280                 285
```

FIG. 6A

```
His Asn Cus Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
    290                 295                 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
305                 310                 315                 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
                325                 330                 335
Cys Val Cys Arg Gly Asn Ala Gly Gly
            340                 345
```

FIG. 6B

FIG.7

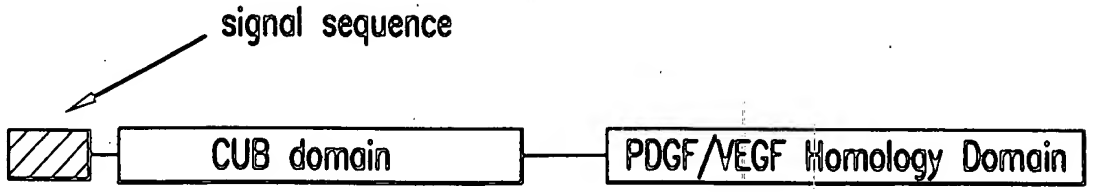


FIG.8

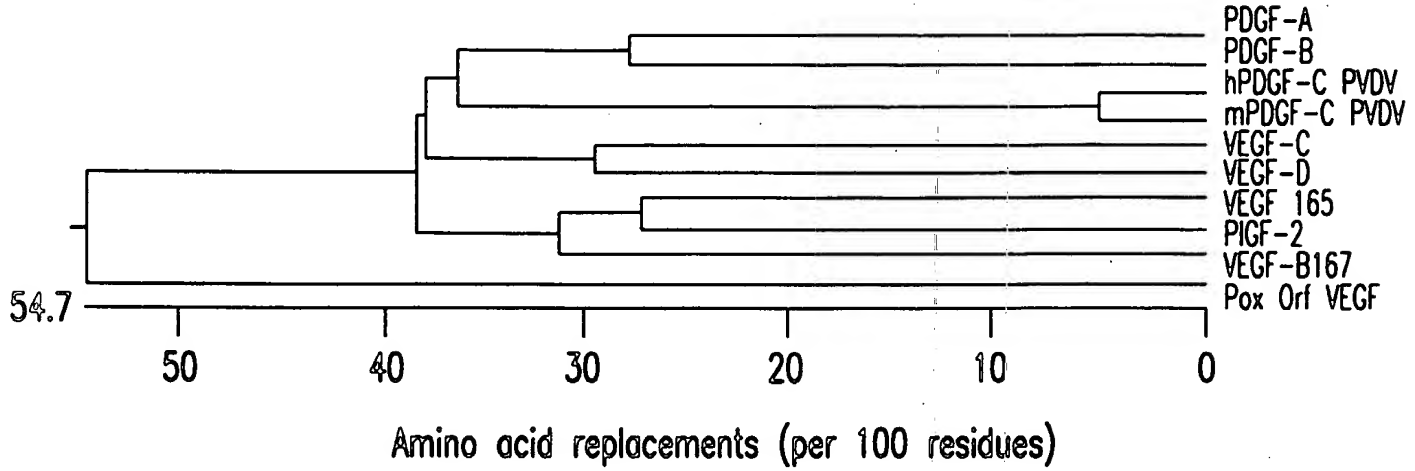


FIG.10

```
VEGF 165        ------------------------------------------------ 1
PIGF-2          ------------------------------------------------ 1
VEGF-B167       ------------------------------------------------ 1
Pgx Crf VEGF    ------------------------------------------------ 1
VEGF-C          MHLLGFFSVACSLLAAALLPGPREAPAAAA 30
VEGF-D          ----------------MYGEWGMGNILMMFH 15
PDGF-A          ------------------------------------------------ 1
PDGF-B          ------------------------------------------------ 1
hPDGF-C PVDV    ------------------------------------------------ 1
mPDGF-C PVDV    ------------------------------------------------ 1

VEGF 165        ------------------------------------------------ 1
PIGF-2          ------------------------------------------------ 1
VEGF-B167       ------------------------------------------------ 1
Pox Orf VEGF    ------------------------------------------------ 1
VEGF-C          AFESGLDLSDAEPDAGEATAYASKDLEEQL 60
VEGF-D          VYLVQGFRSEHGPYKDFSFERSSRSMLERS 45
PDGF-A          ----MRTLACLLLLGCGYLANVLAEEAEIP 26
PDGF-B          MNRCWALFLSLCCYLRLVSAEGDPIPEELY 30
hPDGF-C PVDV    --------MPQFTEAVSPSVLPPSALPLDLL 23
mPDGF-C PVDV    --------MPQVTETTSPSVLPPSALSLDLL 23

VEGF 165        --------------------MNFLLSWVEW 10
PIGF-2          --------------------MPVMRLFPCF 10
VEGF-B167       --------------------MSPLL 5
Pox Orf VEGF    ------------------------------ 1
VEGF-C          RSVSSVDELMTVLYPEYWKMYKCQLRKGGW 90
VEGF-D          EQQIRAASSLEELLQIAHSEDWKLWRCRLK 75
PDGF-A          REVIERLARSQIHSIRDLQRLLEIDSVGSE 56
PDGF-B          EMLSDHSIRSFDDLQRLLHGDP------GEE 55
hPDGF-C PVDV    NNAITAFSTLEDLIRYLEPERWQLDLEDLY 53
mPDGF-C PVDV    NNAVTAFSTLEELIRYLEPDRWQVDLDSLY 53

VEGF 165        SLALLLYLHHAKWSQAAPMAEGGGQNHHEV 40
PIGF-2          LQLLAGLALPAVPPQQWALSAGNGSSEVEV 40
VEGF-B167       RRLLLAALLQLAPAQAPVSQPDAPGHQRKV 35
Pox Orf VEGF    ------MKLLVGILVAVCLHQYLLNADSNT 24
VEGF-C          QHNREQANLNSRTEETIKFAAAHYNTEI-L 119
VEGF-D          LKSLASMDSRSASHRSTRFAATFYDTET-L 104
PDGF-A          DSLDTSLRAHGVH--ATKHVPEKRPLRIRR 84
PDGF-B          DGAELDLNMTRSHSGGELESLARGRRSLGS 85
hPDGF-C PVDV    RPTWQLLGKAFVFGRKSR---------VVDL 75
mPDGF-C PVDV    KPTWQLLGKAFLYGKKSK---------VVNL 75
```

FIG. 9A

```
VEGF 165          VKFMDVYQRSYCHPIETLVDIFQEYPDEIE  70
PIGF-2            VPFQEVWGRSYCRALERLVDVVSEYPSEVE  70
VEGF-B167         VSWIDVYTRATCQPREVVVPLTVELMGTVA  65
Pox Orf VEGF      KGWSEVLKGSECKPRPIVVPVSETHPELTS  54
VEGF-C            KSIDNEWRKTQCMPREVCIDVGKEFGVATN 149
VEGF-D            KVIDEEWDRTQCSPRETCVEVASELGKTTN 134
PDGF-A            KRSIEEAVPAVCKTRTVIYEIPRSQVDPTS 114
PDGF-B            LTIAEPAMIAECKTRTEVFEISRRLIDRTN 115
HPDGF-C PVDV      NLLTEEVRLYSCTPRNFSVSI-REELKRTD 104
mPDGF-C PVDV      NLLKEEVKLYSCTPRNFSVSI-REELKRTD 104

VEGF 165          YIFK--PSCVPLMRCGG---CCNDEGLECV  95
PIGF-2            HMFS--PSCVSLLRCTG---CCGDEDLHCV  95
VEGF-B167         KQLV--PSCVTVQRCGG---CCPDDGLECV  90
Pox Orf VEGF      QRFN--PPCVTLMRCGG---CCNDESLECV  79
VEGF-C            TFFK--PPCVSVYRCGG---CCNSEGLQCM 174
VEGF-D            TFFK--PPCVNVFRCGG---CCNEEGVMCM 159
PDGF-A            ANFLIWPPCVEVKRCTG---CCNTSSVKCQ 141
PDGF-B            ANFLVWPPCVEVQRCSG---CCNNRNVQCR 142
hPDGF-C PVDV      TIF--WPGCLLVKRCGGNCACCLHNCNECQ 132
mPDGF-C PVDV      TIF--WPGCLLVKRCGGNCACCLENCNECQ 132

VEGF 165          PTEESNITMQIMRIK---PHQGQ------HI 117
PIGF-2            PVETANVTMQLLKIR---SGDRP------SY 117
VEGF-B167         PTGQHQVRMQILMIRY--PSSQL------- 111
Pox Orf VEGF      PTEEVNVSMELLGASGSGSNGMQ-----RL 104
VEGF-C            NTSTSYLSKTLFEITV--PLSQG-----PK 197
VEGF-D            NTSTSYISKQLFEISV--PLTSV-----PE 182
PDGF-A            PSRVHHRSVKVAKVEYVRKKPKL-----KE 166
PDGF-B            PTQVQLRPVQVRKLEIVRKKPIF-----KK 167
hPDGF-C PVDV      CVP-SKVTKKYHEVLQLRPKTGVRGLHKSL 161
mPDGF-C PVDV      CVP-RKVTKKYHEVLQLRPKTGVKGLHKSL 161

VEGF 165          GEMSFLQHNK-CECRPKK----------DR 136
PIGF-2            VELTFSQHVR-CECRPLRE----KMKPERR 142
VEGF-B167         GEMSLEEHSQ-CECRPKKK-----DSAVKP 135
Pox OrF VEGF      SFVEHKK----CDCRPRFT--------TTPP 123
VEGF-C            PVTISFANHTSCRCMSKLD---VYRQVHSI 224
VEGF-D            LVPVKIANHTGCKCLPTGP-----RHPYSI 207
PDGF-A            VQVRLEEHLE-CACATTSLNPDYREEDTGR 195
PDGF-B            ATVTLEDHLA-CKCETVAAARPVTRSPGGS 196
hPDGF-C PVDV      TDVALEHHEE-CDCVCRGSTGG         182
mPDGF-C PVDV      TDVALEHHEE-CDCVCRGNAGG         182
```

FIG. 9B

```
VEGF 165      A R Q E N P C G P C S S E R R K H L F V Q D P Q T C K C S C  166
PIGF-2        R P K G R G K R R R E N Q R P T D C H L C G D A V P R R     170
VEGF-B167     D S P R P L C P R C T Q H H Q R P D P R T - - - - C R C R C  161
Pox Orf VEGF  T T T R P P R R R R                                        133
VEGF-C        I R R S L R A T - L P Q C Q A A N K T C P T N Y M W N N H I  253
VEGF-D        I R R S L Q T P E E D E C P H S K K L C P I D M L W D N T K  236
PDGF-A        P R E S G K K R K R K R L K P T                             211
PDGF-B        Q E Q R A K T P Q T R V T I R T V R V R R P P K G K H R K F  225
hPDGF-C PVDV                                                             182
mPDGF-C PVDV                                                             182

VEGF 165      K N T D S - R C K A R Q L E L N E R T C R C D K P R R      192
PIGF-2                                                                   170
VEGF-B167     R R R S F L R C Q G R G L E L N P D T C R C R K L R R      188
Pox Orf VEGF                                                             133
VEGF-C        C R C L A Q E D F M F S S D A G D D S T D G F H D I C G P N  283
VEGF-D        C K C V L Q D E - T P L P G T E D H S Y L Q E P T L C G P H  266
PDGF-A                                                                   211
PDGF-B        K H T H D K T A L K E T L G A                              241
hPDGF-C PVDV                                                             182
mPDGF-C PVDV                                                             182

VEGF 165                                                                 192
PIGf-2                                                                   170
VEGF-B167                                                                188
Pox Orf VEGF                                                             133
VEGF-C        K E L D E E T C Q C V C R A G L R P A S C G P H K E L D R N  313
VAGF-D        M T F D E D R - - - - - - - - - - - - - - - - - - - - - -  273
PDGF-A                                                                   211
PDGF-B                                                                   241
hPDGF-C PVDV                                                             182
mPDGF-C PVDV                                                             182

VEGF 165                                                                 192
PIGF-2                                                                   170
VEGF-B167                                                                188
Pox Orf VEGF                                                             133
VEGF-C        S C Q C V C K N K L F P S Q C G A N R E F D E N T C Q C V C  343
VEGF-D        - C E C V C K A P C P G D L I Q H P E N - - - - - C S C F E  297
PDGF-A                                                                   211
PDGF-B                                                                   241
hPDGF-C PVDV                                                             182
mPDGF-C PVDV                                                             182
```

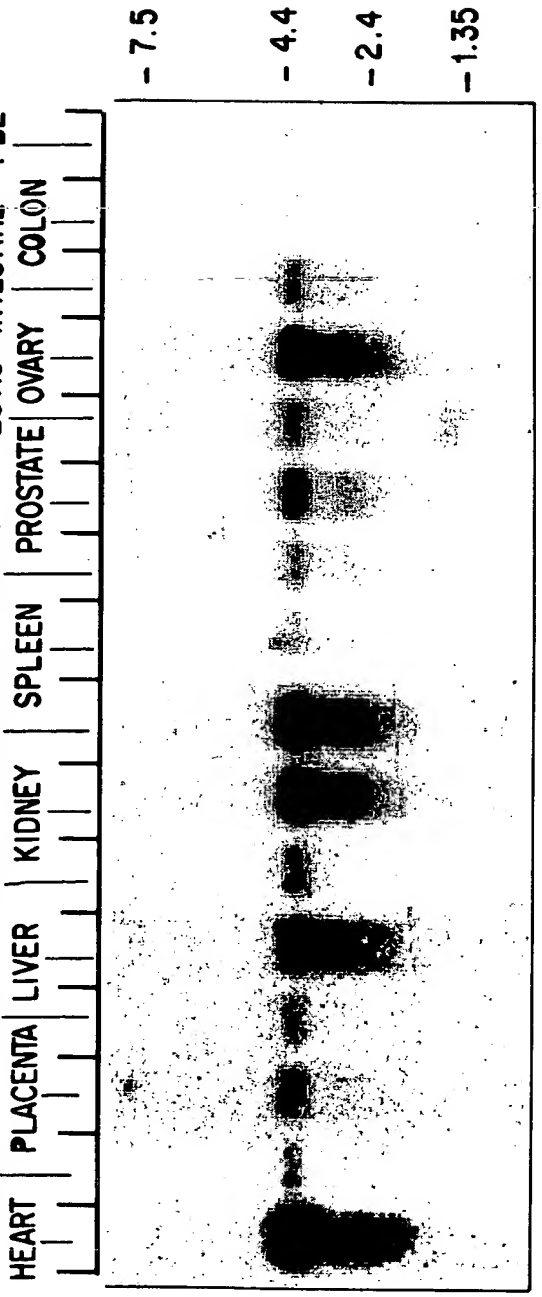
FIG. 9C

```
VEGF 165                                                                    192
PIGF-2                                                                      170
VEGF-B167                                                                   188
Pox Orf VEGF                                                                133
VEGF-C          K R T C P R N Q P L N P G K C A C E C T E S P Q K C L L K G  373
VEGF-D          C K E S L E S C C O K K K I- - - - - - - - - - - - - - - -  312
PDGF-A                                                                      211
PDGF-B                                                                      241
hPDGF-C PVDV                                                                182
mPDGF-C PVDV                                                                182

VEGF 165                                                                    192
PIGF-2                                                                      170
VEGF-B167                                                                   188
Pox Orf VEGF                                                                133
VEGF-C          K K F H H Q T C S C Y R R P C T N R Q K A C E P G F S Y S E  403
VEGF-D          - - F H P D T C S C E D R - C P F H T R T C A S R K P A C G  338
PDGF-A                                                                      211
PDGF-B                                                                      241
hPDGF-C PVDV                                                                182
mPDGF-C PVDV                                                                182

VEGF 165                                                                    192
PIGF-2                                                                      170
VEGF-B167                                                                   188
Pox Orf VEGF                                                                133
VEGF-C          E V C R C V P S Y W K R P Q M S                             419
VEGF-D          K H W R F P K E T R A Q G L Y S O E N P                     358
PDGF-A                                                                      211
PDGF-B                                                                      241
hPDGF-C PVDV                                                                182
mPDGF-C PVDV                                                                182
```

FIG. 9D

FIG. 11

FIG. 12


HEART
BRAIN
PLACENTA
LUNG
LIVER
SKELETAL MUSCLE
KIDNEY
PANCREAS
SPLEEN
THYMUS
PROSTATE
TESTIS
OVARY
SM. INTESTINE
COLON
PBL
7.5
4.4
2.4
1.35

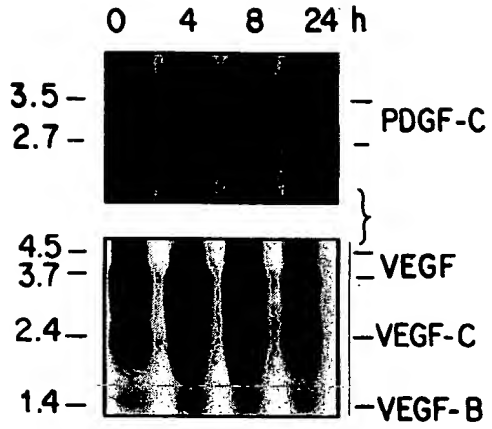

0 4 8 24 h
3.5
2.7
PDGF-C
4.5
3.7
VEGF
2.4
VEGF-C
1.4
VEGF-B

FIG. 13

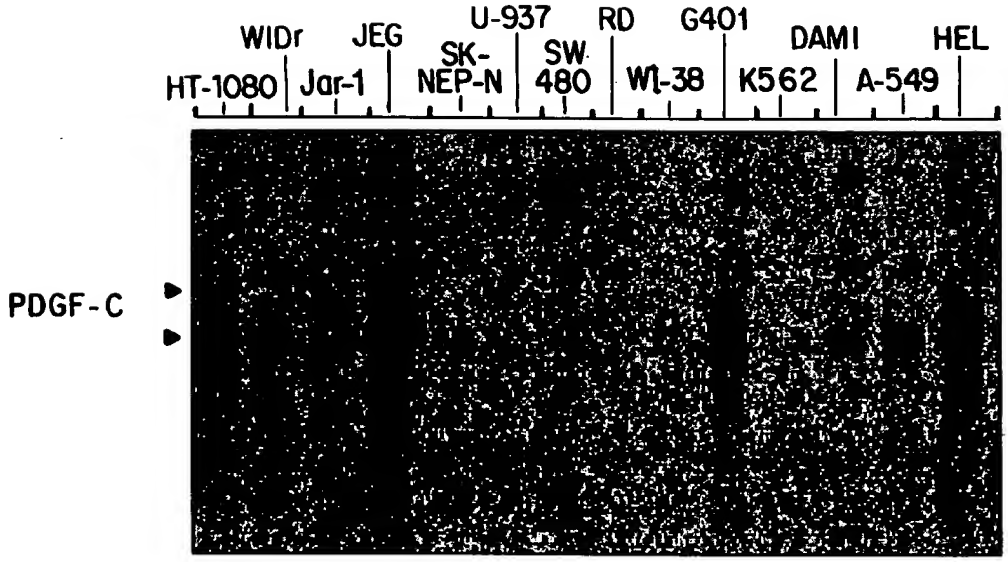

WIDr
JEG
U-937
RD
G401
DAMI
HEL
HT-1080
Jar-1
SK-NEP-N
SW 480
Wi-38
K562
A-549
PDGF-C

FIG. 14

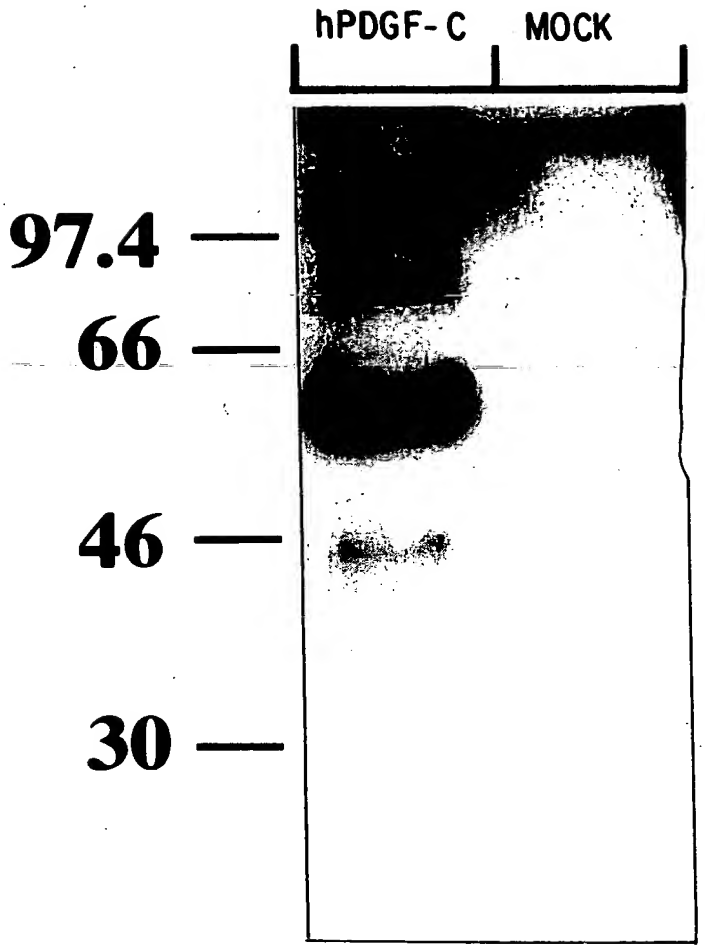


FIG. 15

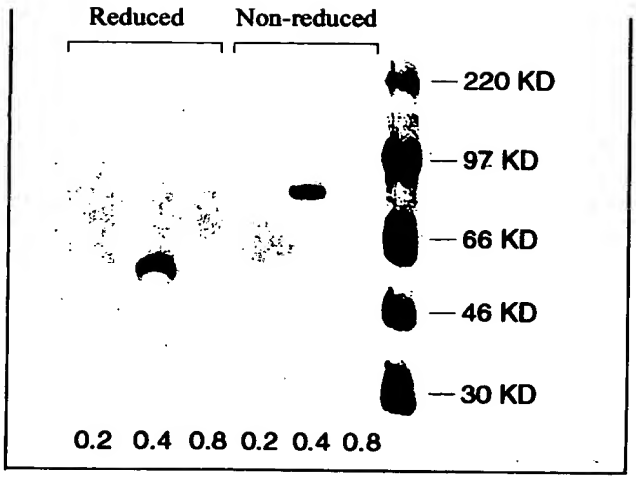


FIG. 16A

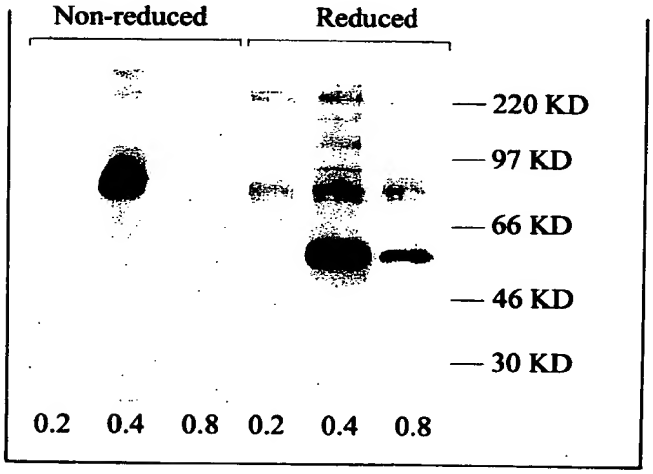


FIG. 16B

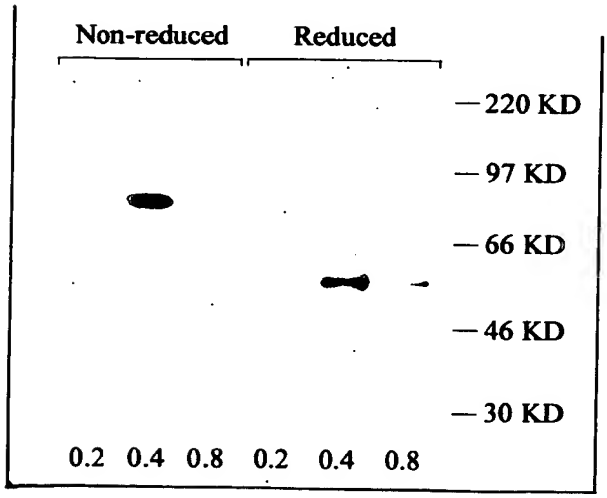


FIG. 16C

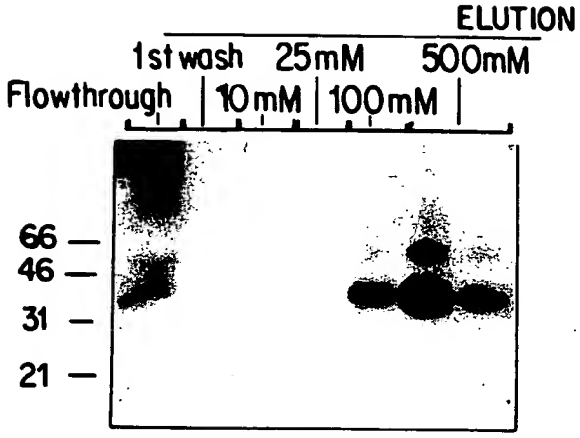


FIG. 17A

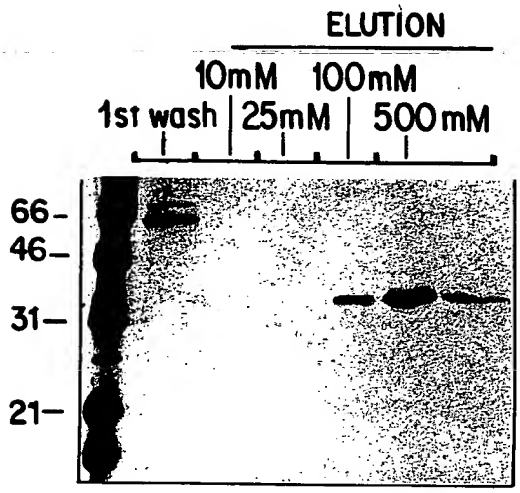


FIG. 17B

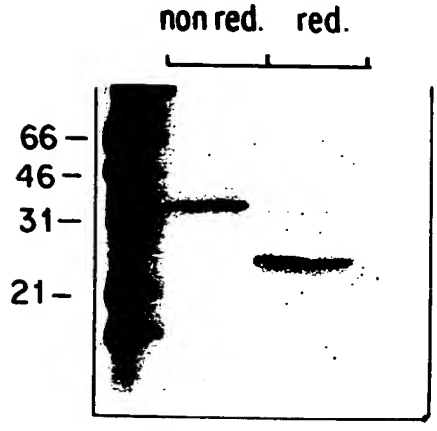


FIG. 17C

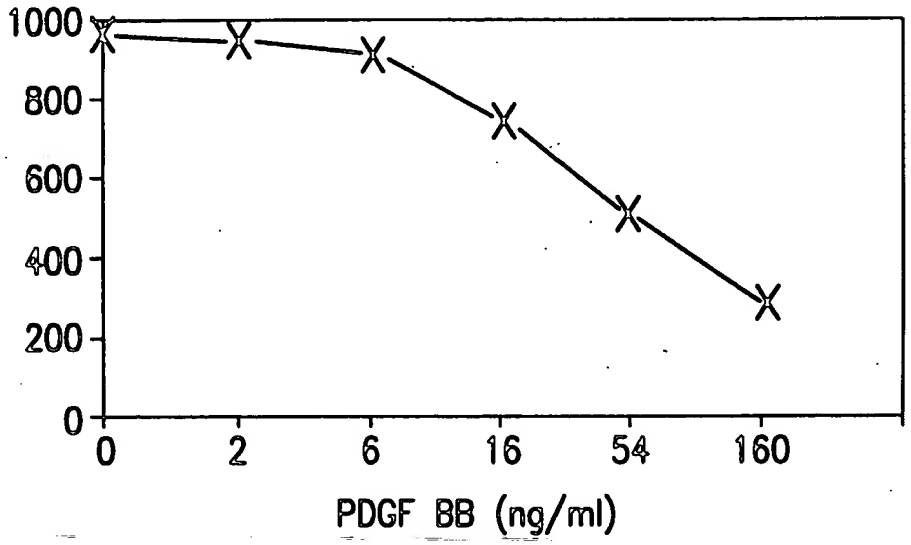

1000
800
600
400
200
0
0
2
6
16
54
160
PDGF BB (ng/ml)

FIG. 18

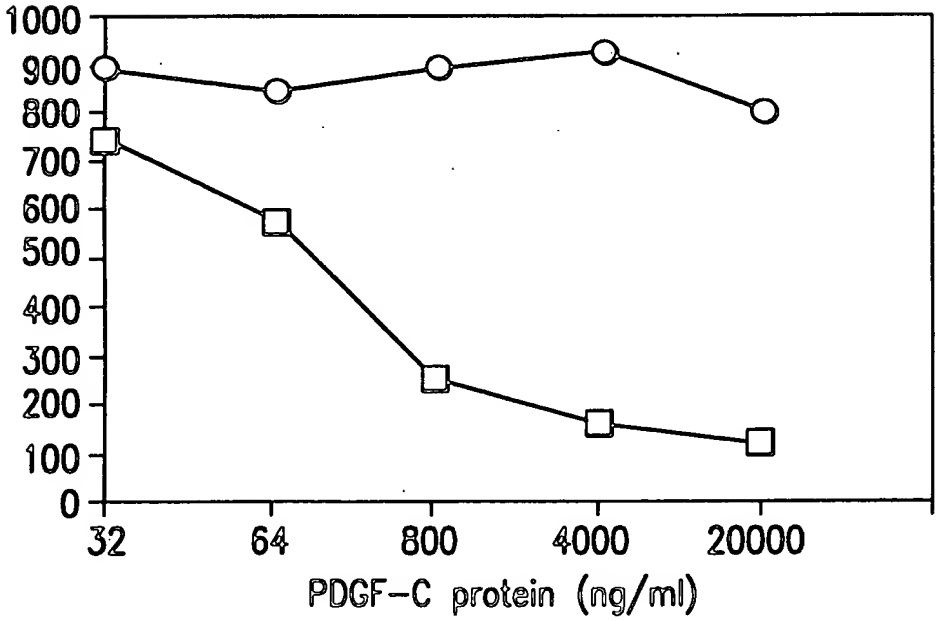
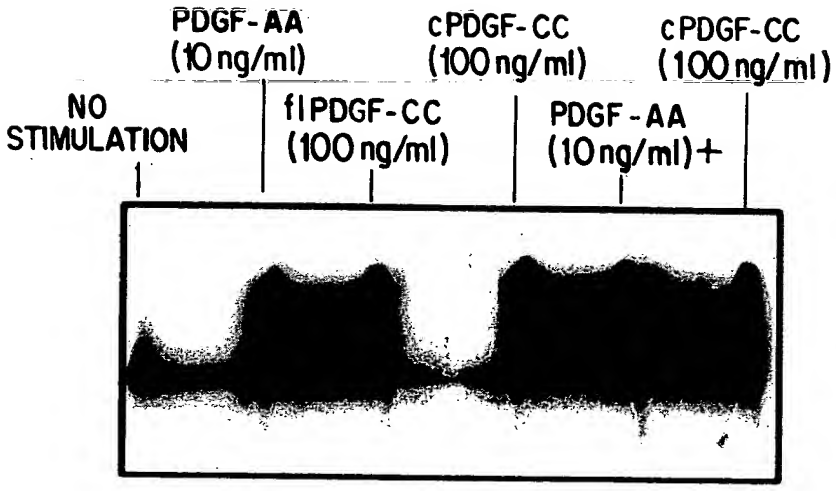

1000
900
800
700
600
500
400
300
200
100
0
32
64
800
4000
20000
PDGF-C protein (ng/ml)

FIG. 19



IP : PDGF alpha-rec.
IB: P-T yr

FIG. 20

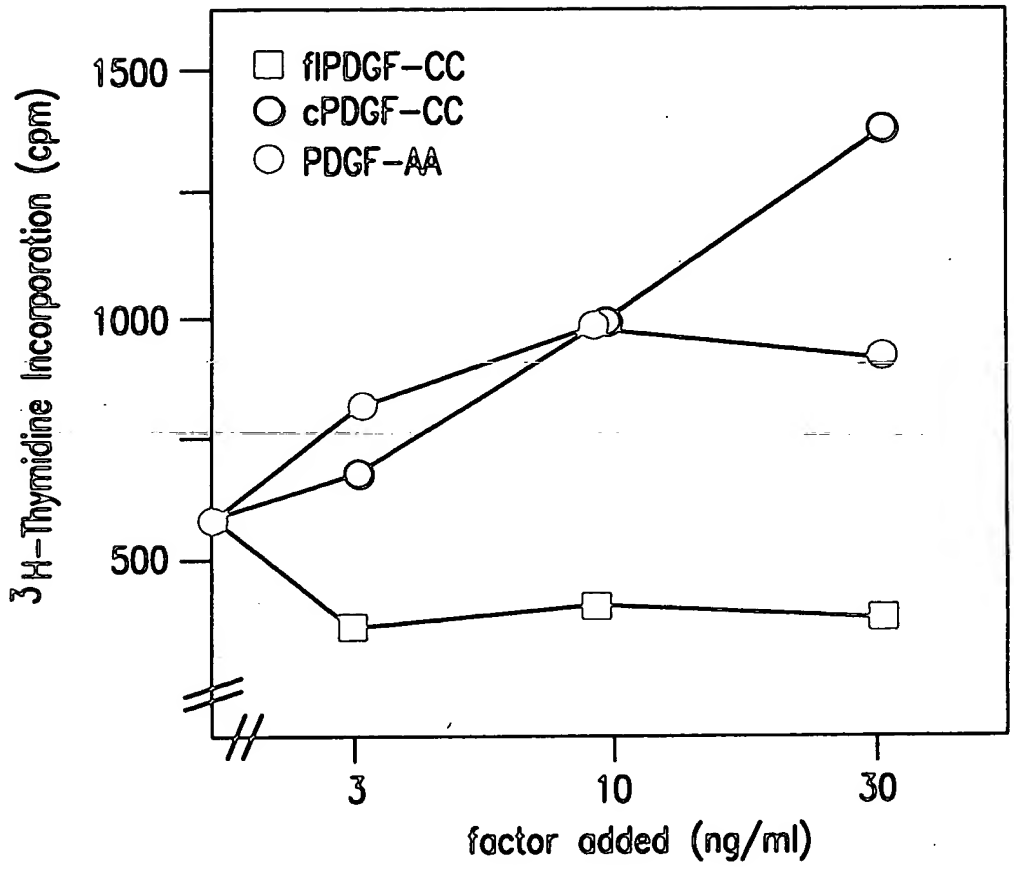

flPDGF-CC
cPDGF-CC
PDGF-AA
1500
1000
500
^{3}H-Thymidine Incorporation (cpm)
3
10
30
factor added (ng/ml)

FIG. 21

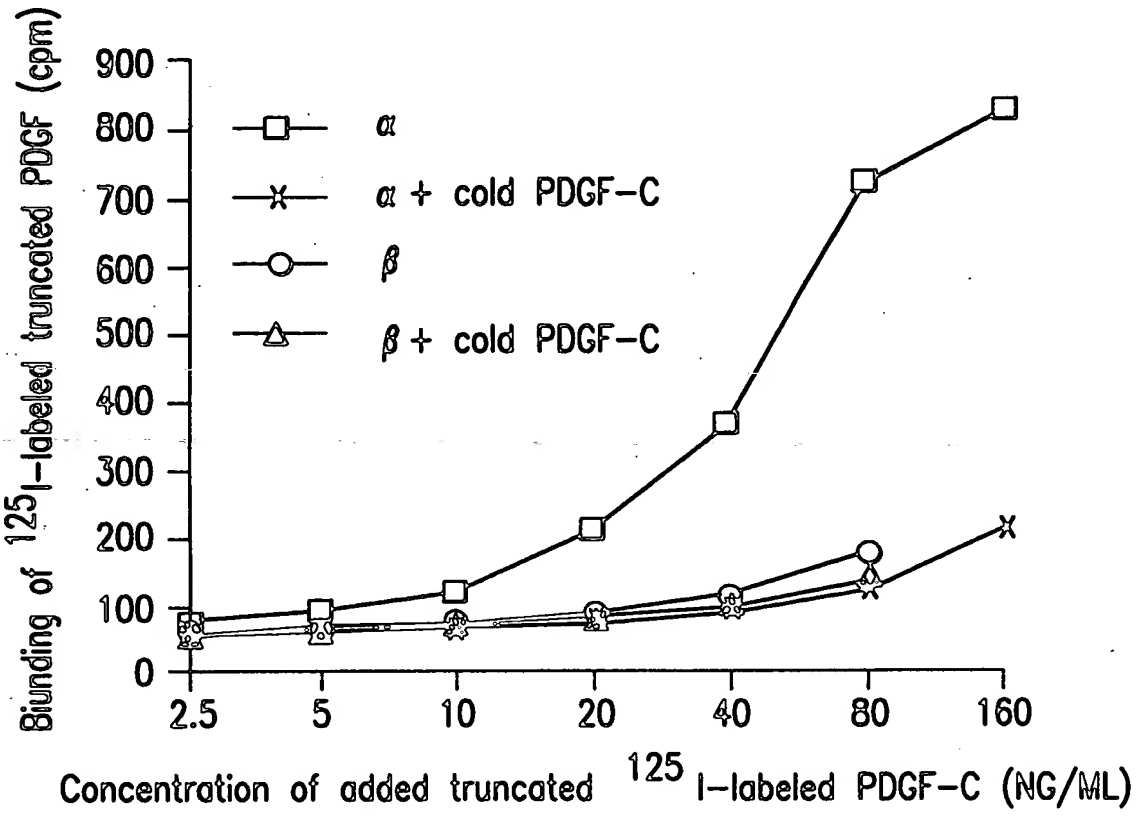

Binding of 125I-labeled truncated PDGF (cpm)
900
800
700
600
500
400
300
200
100
0
α
α + cold PDGF-C
β
β + cold PDGF-C
2.5
5
10
20
40
80
160
Concentration of added truncated 125 I-labeled PDGF-C (NG/ML)

FIG. 22

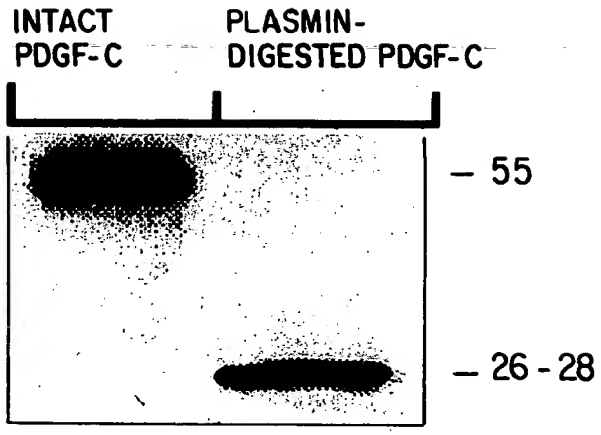


FIG. 23

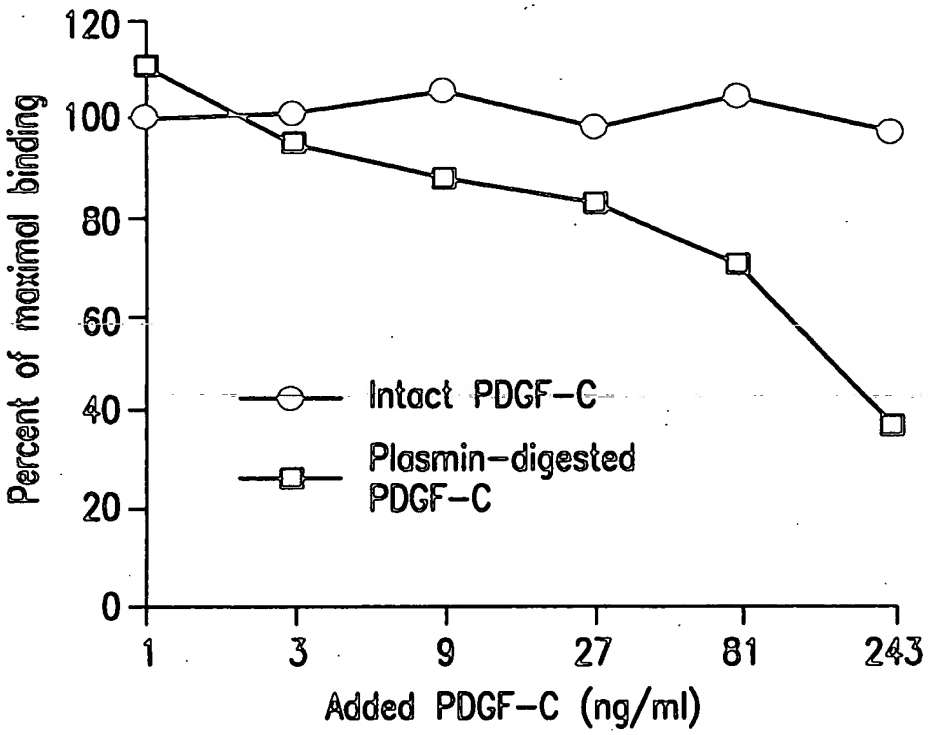

120
100
80
60
40
20
0
Percent of maximal binding
Intact PDGF-C
Plasmin-digested PDGF-C
1
3
9
27
81
243
Added PDGF-C (ng/ml)

FIG. 24

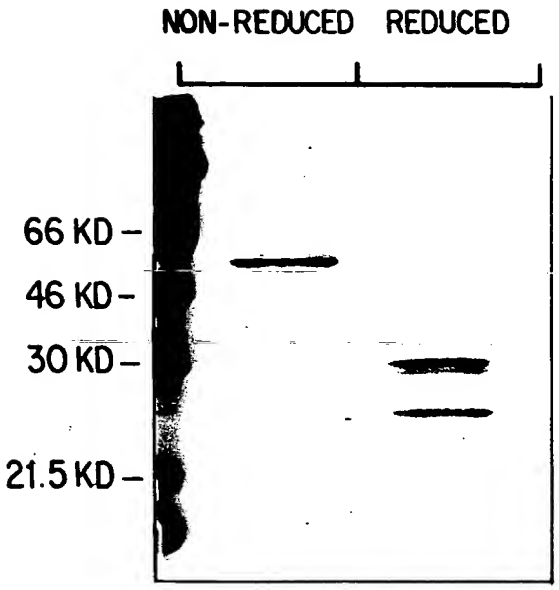


FIG. 25

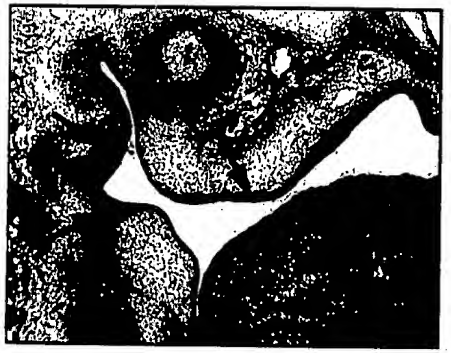


FIG. 26A

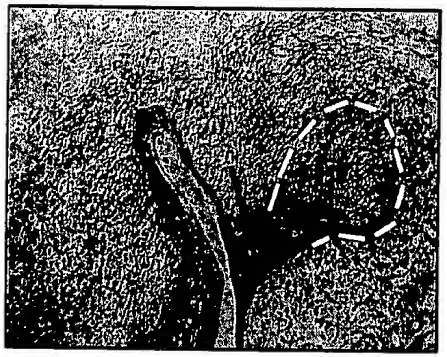


FIG. 26B

FIG. 26C

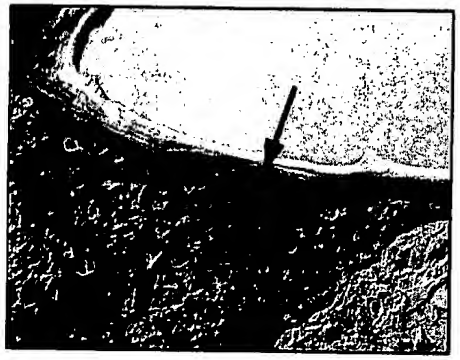


FIG. 26D

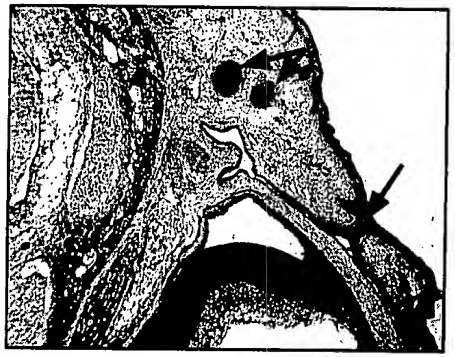


FIG. 26E

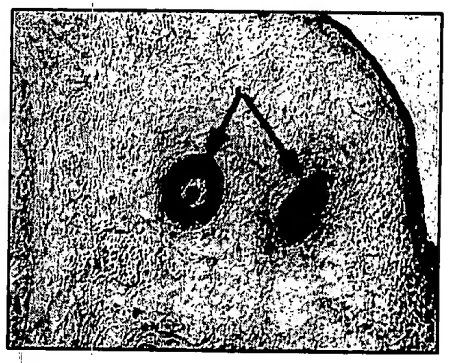


FIG. 26F

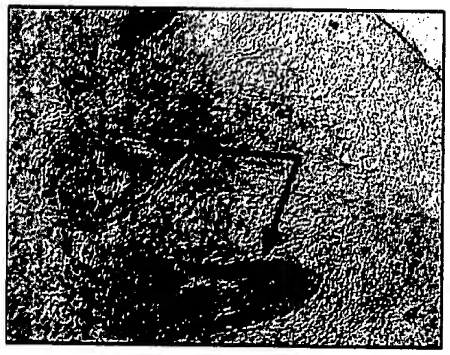


FIG. 26G

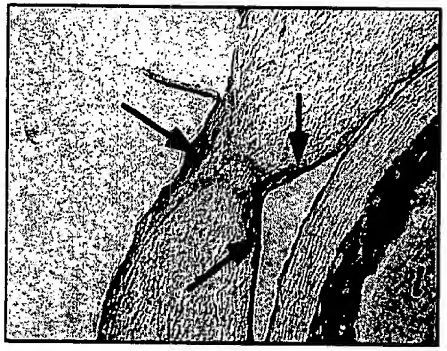


FIG. 26H

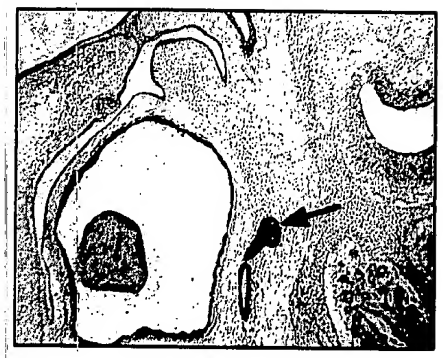


FIG. 26I

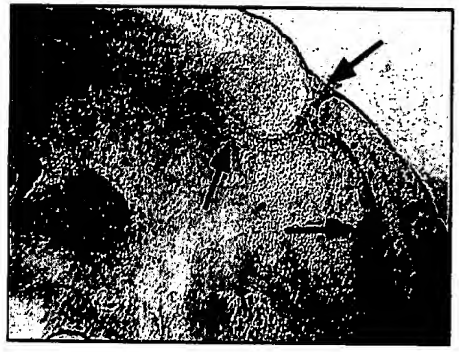


FIG. 26J

FIG. 26K

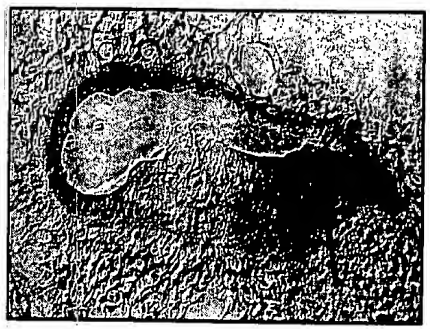


FIG. 26L

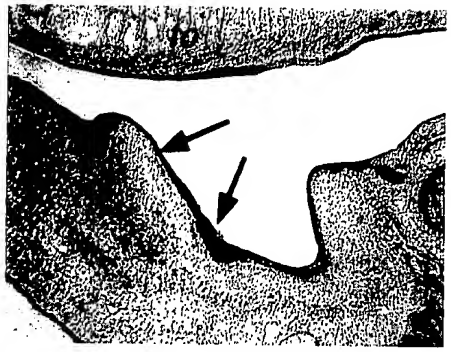


FIG. 26M

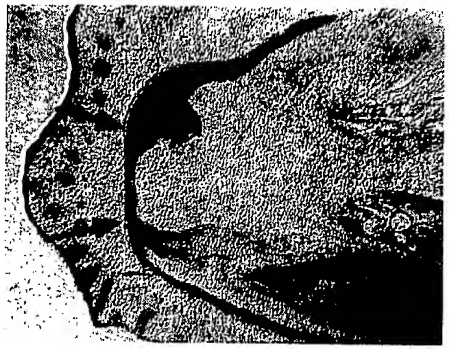


FIG. 26N

FIG. 26O

FIG. 26P

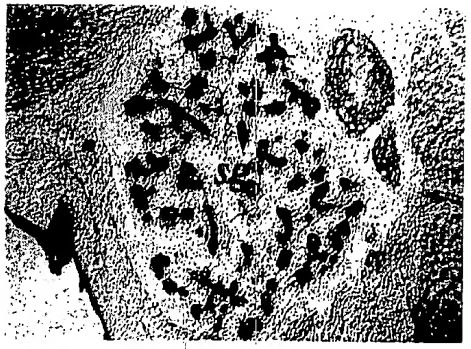


FIG. 26Q

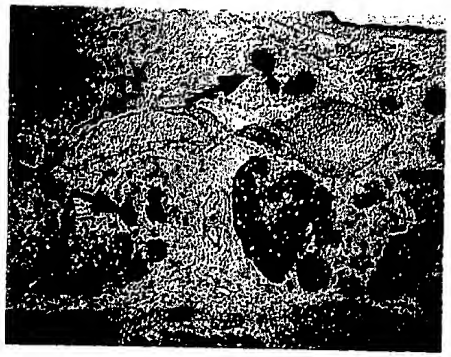


FIG. 26 R

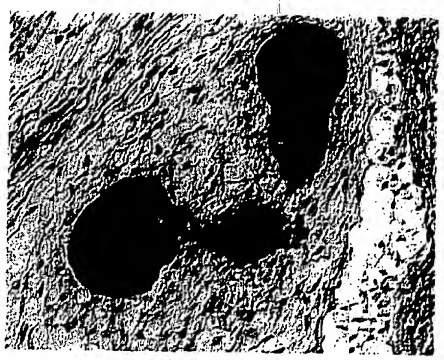


FIG. 26S

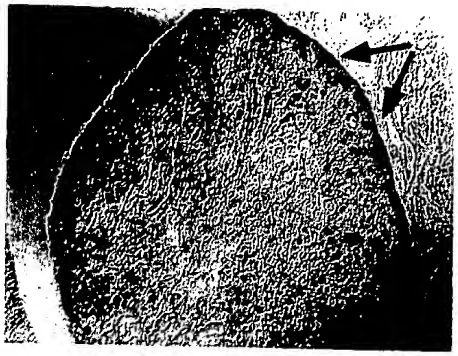


FIG. 26T

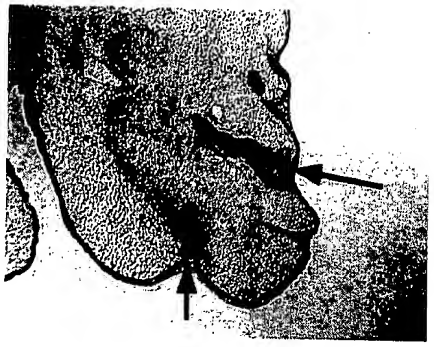


FIG. 26U

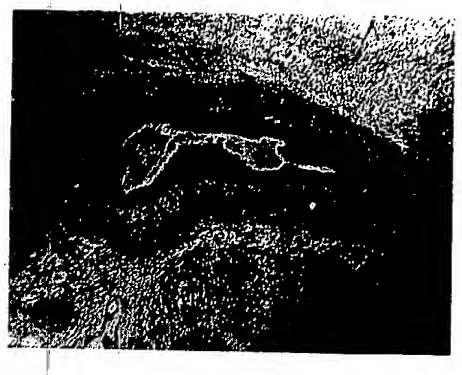


FIG. 26V

FIG. 27A

FIG. 27B

FIG. 27C

FIG. 27D

FIG.27E

FIG. 27F

FIG. 28B

FIG. 28D

FIG. 28A

FIG. 28C

FIG. 28F

FIG. 28E

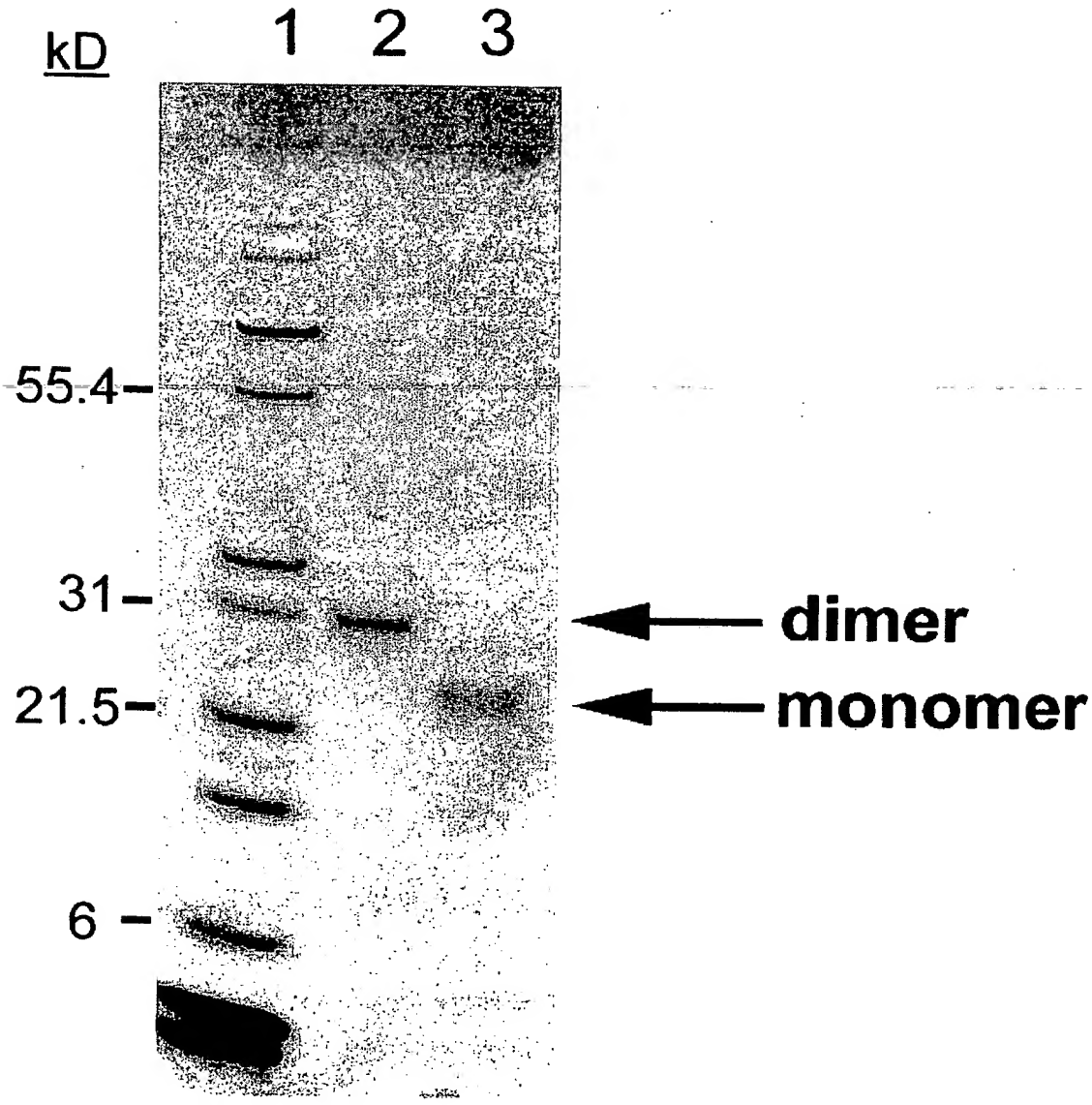


FIG. 29

FIG. 30A

FIG. 30B

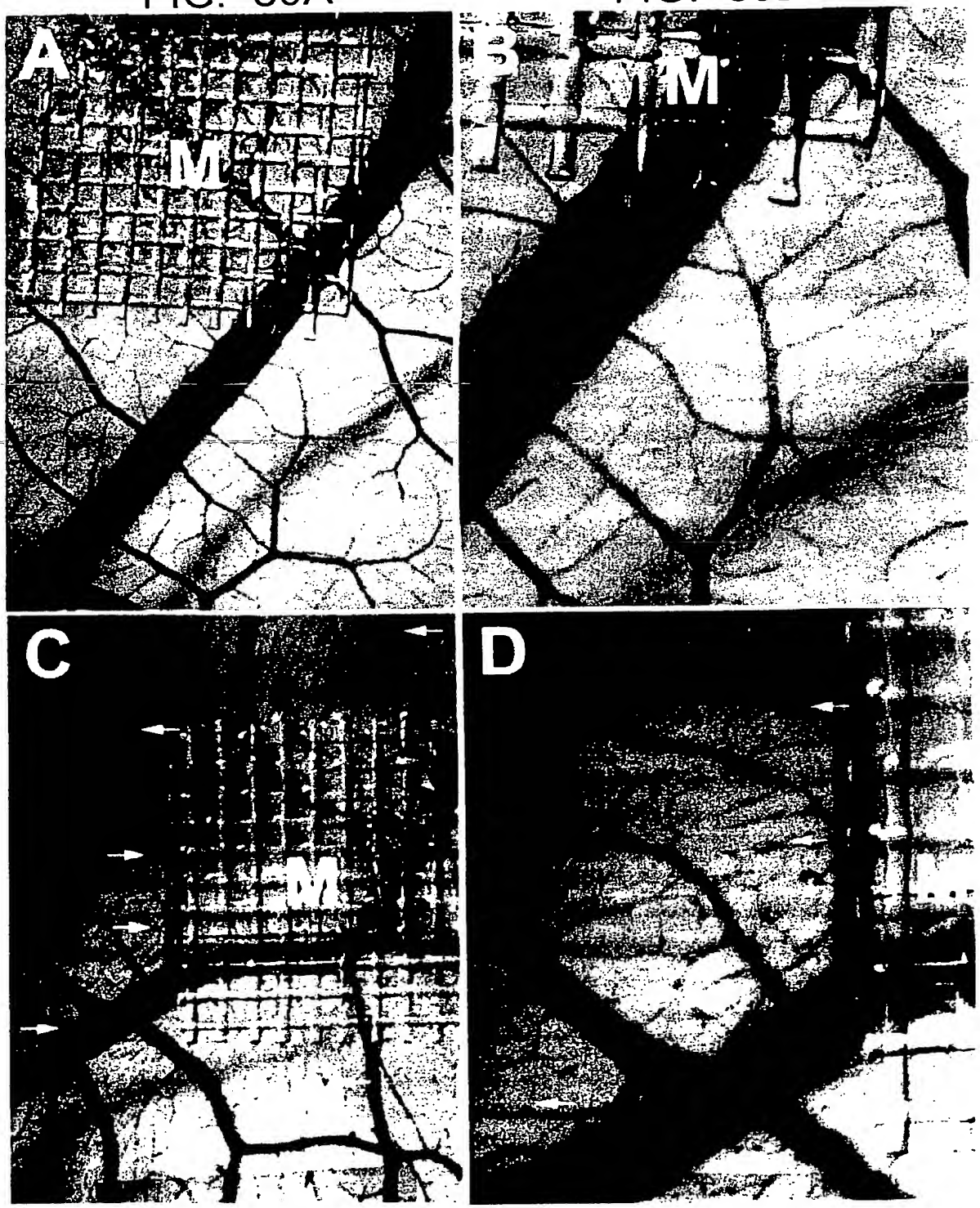


FIG. 30C

FIG. 30D

FIG. 31A

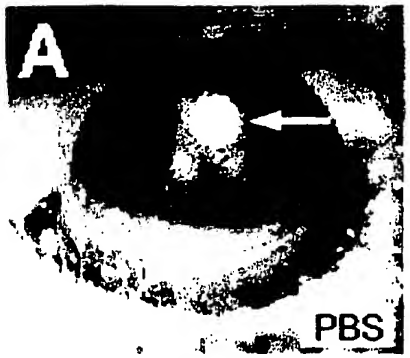


FIG. 31B

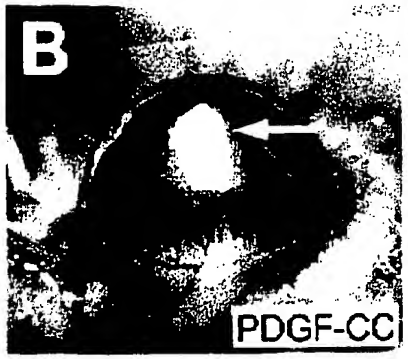


FIG. 31C

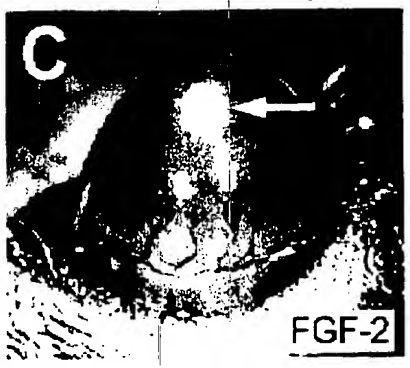
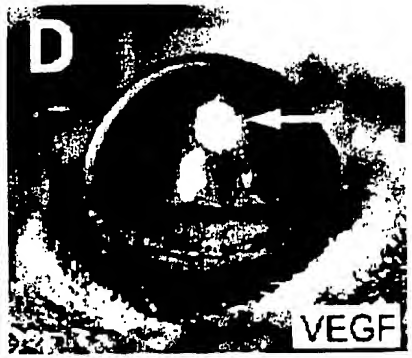


FIG. 31D



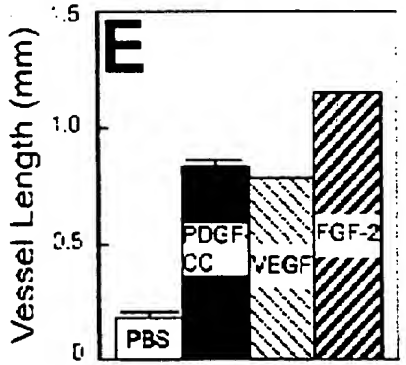


FIG. 31E

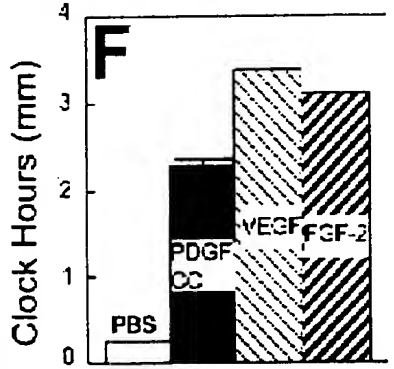


FIG. 31F

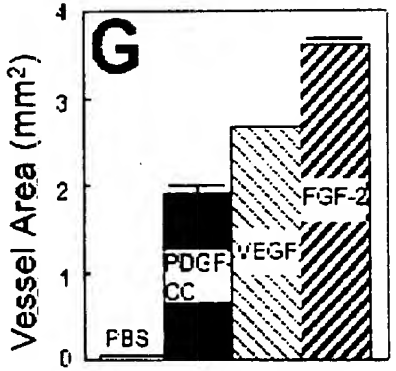


FIG. 31G

FIG. 32A

FIG. 32B

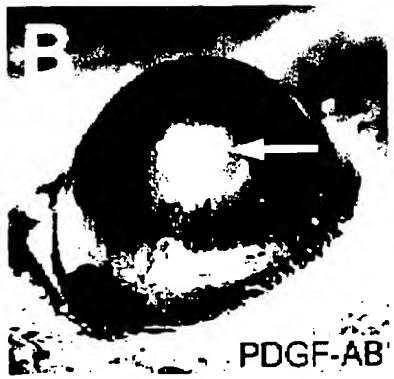


FIG. 32C

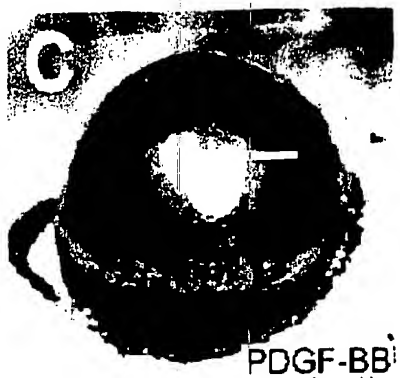
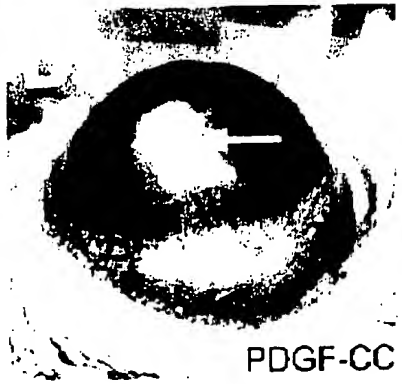


FIG. 32D



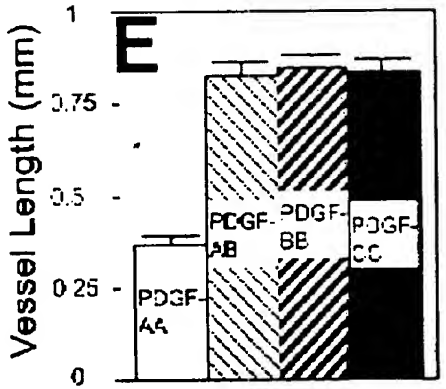


FIG. 32E

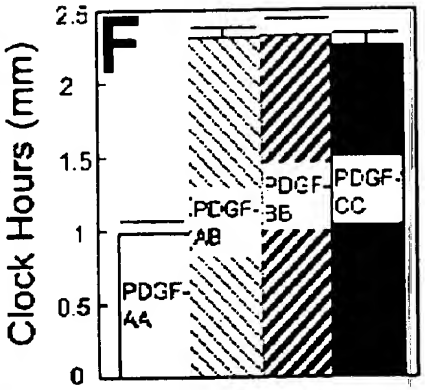


FIG. 32F

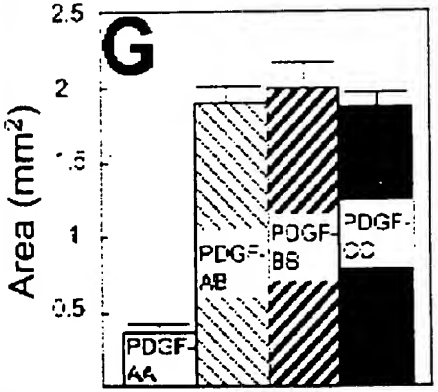


FIG. 32G

FIG. 33A

FIG. 33B

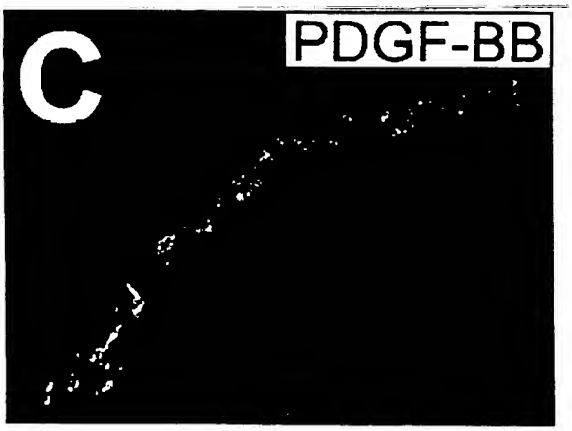


FIG. 33C

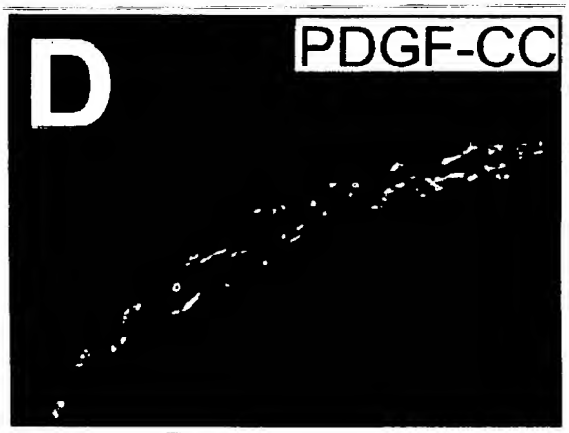


FIG. 33D

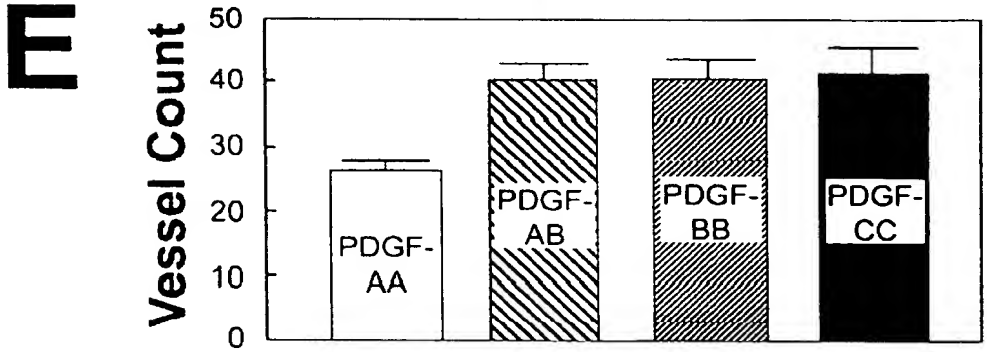


FIG. 33E